ENTERED

PCT10

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/088,046

DATE: 04/04/2002
TIME: 15:38:34

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\04042002\J088046.raw

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     4 <110> APPLICANT: Joelle Thonnard
     6 <120> TITLE OF INVENTION: Novel Compounds
     9 <130> FILE REFERENCE: BM45414
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/088,046
C--> 11 <141> CURRENT FILING DATE: 2002-03-14
    11 <150> PRIOR APPLICATION NUMBER: 9921694.7
    12 <151> PRIOR FILING DATE: 1999-09-14
    14 <150> PRIOR APPLICATION NUMBER: 9921693.9
    15 <151> PRIOR FILING DATE: 1999-09-14
    17 <150> PRIOR APPLICATION NUMBER: 9922829.8
    18 <151> PRIOR FILING DATE: 1999-09-25
    20 <160> NUMBER OF SEQ ID NOS: 6
    22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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    25 <211> LENGTH: 1035
    26 <212> TYPE: DNA
    27 <213> ORGANISM: Moraxella catarrhalis
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    31 ctaaatgcac atgcagcacc tgaattatat ggttacgcaa atcttgtcgt ttctgctaat       120
    32 cataaaaaaa caaccaacaa gacaaccaat gtcagtacat caacaacaga ccgcccctat       180
    33 ctgtatagca gcggatcacg cattggcctt agagggtctg aaaagttaaa tgatgattat       240
    34 gaggttttgt acaagttgga gtaccgtcta gaaaatgatg gtgatttacg caatgaaaaa       300
    35 atcaagcagc cagatggtac tgaaaagact gttgctaaaa cacgcaattt tgaggctcgt       360
    36 gattcatgga ttggcgtgaa gcataaaaag tatggtacca tcaaggcggg tcgtatgttg       420
    37 tctttggatc catatgtgcg ttatactgcc tatttggcgt caggcgtaga tggggtgcgt       480
    38 accaataata ccattgcata cgaatcacca aaaatcaaag atgttagttt tcaggcgatg       540
    39 tacatcttag atgaaaataa agagacagat accattgatc gtgatggtta ttcattgctt       600
    40 gtcaagaaaa acacagatac atataatgtt ggtgcagctt atgcctattt tggtaaagca       660
    41 aaaacctctt atggcaagat taactatact gcgcgtgtga caggtaatta taaaattaat       720
    42 gaggattata agtaggtgg tatctatcag catgtcggct atgccaatga cgacagtgcc       780
    43 aaaaataata cagaacaagc tgttggcgtg gctttgcagc attttaaaga caaatggact       840
    44 cataccgcac acatgaatct tgtgaataat cctagtggga aaagggcga tgggtttgag       900
    45 ctgatcggag caattgaccg tgatatttct aaaaatgtct ctgcaggcat ggatatcacc       960
    46 tatggtaact ttaactacgc aacagaaaaa gaatcttaca tcaacccaac tatctatgcg      1020
    47 actgtatatt tttaa                                                       1035
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    50 <211> LENGTH: 344
    51 <212> TYPE: PRT
    52 <213> ORGANISM: Moraxella catarrhalis
    54 <400> SEQUENCE: 2
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    56 1               5                   10                  15
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57 Gly Gly Met Met Leu Asn Ala His Ala Ala Pro Glu Leu Tyr Gly Tyr
58            20              25            30
59 Ala Asn Leu Val Val Ser Ala Asn His Lys Lys Thr Thr Asn Lys Thr
60            35              40              45
61 Thr Asn Val Ser Thr Ser Thr Thr Asp Arg Pro Tyr Leu Tyr Ser Ser
62     50              55              60
63 Gly Ser Arg Ile Gly Leu Arg Gly Ser Glu Lys Leu Asn Asp Asp Tyr
64 65              70              75              80
65 Glu Val Leu Tyr Lys Leu Glu Tyr Arg Leu Glu Asn Asp Gly Asp Leu
66            85              90              95
67 Arg Asn Glu Lys Ile Lys Gln Pro Asp Gly Thr Glu Lys Thr Val Ala
68            100             105             110
69 Lys Thr Arg Asn Phe Glu Ala Arg Asp Ser Trp Ile Gly Val Lys His
70            115             120             125
71 Lys Lys Tyr Gly Thr Ile Lys Ala Gly Arg Met Leu Ser Leu Asp Pro
72     130             135             140
73 Tyr Val Arg Tyr Thr Ala Tyr Leu Ala Ser Gly Val Asp Gly Val Arg
74 145             150             155             160
75 Thr Asn Asn Thr Ile Ala Tyr Glu Ser Pro Lys Ile Lys Asp Val Ser
76            165             170             175
77 Phe Gln Ala Met Tyr Ile Leu Asp Glu Asn Lys Glu Thr Asp Thr Ile
78            180             185             190
79 Asp Arg Asp Gly Tyr Ser Leu Leu Val Lys Lys Asn Thr Asp Thr Tyr
80            195             200             205
81 Asn Val Gly Ala Ala Tyr Ala Tyr Phe Gly Lys Ala Lys Thr Ser Tyr
82     210             215             220
83 Gly Lys Ile Asn Tyr Thr Ala Arg Val Thr Gly Asn Tyr Lys Ile Asn
84 225             230             235             240
85 Glu Asp Tyr Lys Val Gly Gly Ile Tyr Gln His Val Gly Tyr Ala Asn
86            245             250             255
87 Asp Asp Ser Ala Lys Asn Asn Thr Glu Gln Ala Val Gly Val Ala Leu
88            260             265             270
89 Gln His Phe Lys Asp Lys Trp Thr His Thr Ala His Met Asn Leu Val
90            275             280             285
91 Asn Asn Pro Ser Gly Lys Lys Gly Asp Gly Phe Glu Leu Ile Gly Ala
92     290             295             300
93 Ile Asp Arg Asp Ile Ser Lys Asn Val Ser Ala Gly Met Asp Ile Thr
94 305             310             315             320
95 Tyr Gly Asn Phe Asn Tyr Ala Thr Glu Lys Glu Ser Tyr Ile Asn Pro
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97 Thr Ile Tyr Ala Thr Val Tyr Phe
98            340
100 <210> SEQ ID NO: 3
101 <211> LENGTH: 2037
102 <212> TYPE: DNA
103 <213> ORGANISM: Moraxella catarrhalis
105 <400> SEQUENCE: 3
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107 gtggccaaag ctcagattgc accagaccca accaaagcaa atctttctgc aataaccgat      120
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PATENT APPLICATION: US/10/088,046

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108 gatcgtcgtc aggcggctct tgcacattta gcaagacaag atttggcagc aacagatgac    180
109 gacatgggtg tcgatatcaa tcaaaccaat atcaaccagc caaattggca agatgacaag    240
110 aatggcgatt catgtttttt ggttgatgag attgactttg tgattgaggg tggagaagat    300
111 aaacatattc taggtatgac gccgagcaat ttacgcagct tgctatcgcc cctgttggac    360
112 cggacaaagc caacatatgc tcttaatcac tgcatcaaca atcacaacct atctttaatt    420
113 gtagatattg cccataatga attactaaag cgtggttatt taactagcag tattagcatt    480
114 gaagagcagg atttatcaac taaaaaactc actttaacag tccatgctgg caaggtgaaa    540
115 aaggtgatat tggccgatgc tagcaaaacg ccaacttatg tcaaagccgc cattcctctt    600
116 aagttcaatc aagcctttcg tctgtcatat ttagaacaag gtctagataa tttaaaacgc    660
117 atcgatccaa cggcaaccgt gcagattata ccaagcagct ccagtaatgt cgccaatgat    720
118 attgacatta acaccacaaa ccttggtttt agtgatttac tcattaggat ggaccgcagt    780
119 caaagcgctg tatttggcat taatattgat aacagtttat ccaaagatta tggcaattat    840
120 ctgatttctg ctaatgttcg tgctaacaac ctcatgcatc ttaacgatga atggaatctt    900
121 tctgccaact atccattggc gcgcctgatt gacgctgccc aaaatgatct tggggttcag    960
122 gtgggcaagg ataggcaggt taattatcac gcttccttga ctattcctta tggattgtat   1020
123 aaattttctg ccacacacag ccaccaccaa taccagcaat ttcttgaagg gcttcatgcg   1080
124 cccttgactt atcatggcac cagcaagaca agctcaattg gattgtctcg tttattgcac   1140
125 cgtgatggca atcaaaagac tgaaggttat ataaaggtta atcacaaacg aagcagtaat   1200
126 tatattgatg atgttaatct tgaagtgcaa aaccgccgca caacaggata taacattggc   1260
127 atcactcatc agcatcatct tcaccaaggt ggttatttgt atgccaactt ggattataag   1320
128 caaggaacag gggcactaaa agcaaagcct gcacctgaag agcatattta tgatgctttt   1380
129 gggcgacaac tacccagtga gggttttgca aaagcaccaa tttggtcact atacaccagt   1440
130 ttccaaaagc catttgtgtt aaacaaccca aatgatactg aacaagcgca agataaagca   1500
131 acagcaaata aacccattta cacatccatt cctctcactt atactgctag attacaagcc   1560
132 caatatgcca aacaacttcc tgtaccatct gatttattct atttgggtgg cagatatagc   1620
133 attaaaggca ttaaagaggg aaattatttа tcaggagaac atggctttag cctatcccaa   1680
134 gaacttgctt ggcaattgcc attacagaat cttaatcagc actttagtac aaatgcaaac   1740
135 agcgcccagt tgtatgcaag tattgatcaa ggctatgcct atggaaaaaa cactcttaat   1800
136 aatcaacgcc atatcttggc tggagcggtt ggtatgaggt attattttca aggcagtcaa   1860
137 gatccaagaa ttcaagaaac acaaaatggc ttgactcatt tcaaagaatc aaatacttat   1920
138 ctaaataaca caccaaccac agctcatttg gatatattca ttggaaaagg aattaagacg   1980
139 cctgaattta tgaagaaaga aaccgtcgtg ggtgtgagtg ccagcattga gtttttaa     2037
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142 <211> LENGTH: 678
143 <212> TYPE: PRT
144 <213> ORGANISM: Moraxella catarrhalis
146 <400> SEQUENCE: 4
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149 Ser Ile Phe Ser Val Ala Lys Ala Gln Ile Ala Pro Asp Pro Thr Lys
150             20                  25                  30
151 Ala Asn Leu Ser Ala Ile Thr Asp Asp Arg Arg Gln Ala Ala Leu Ala
152         35                  40                  45
153 His Leu Ala Arg Gln Asp Leu Ala Ala Thr Asp Asp Met Gly Val
154     50                  55                  60
155 Asp Ile Asn Gln Thr Asn Ile Asn Gln Pro Asn Trp Gln Asp Asp Lys
156 65                  70                  75                  80
157 Asn Gly Asp Ser Cys Phe Leu Val Asp Glu Ile Asp Phe Val Ile Glu
158             85                  90                  95
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159 Gly Gly Glu Asp Lys His Ile Leu Gly Met Thr Pro Ser Asn Leu Arg
160             100             105             110
161 Ser Leu Leu Ser Pro Leu Leu Asp Arg Thr Lys Pro Thr Tyr Ala Leu
162         115             120             125
163 Asn His Cys Ile Asn Asn His Asn Leu Ser Leu Ile Val Asp Ile Ala
164     130             135             140
165 His Asn Glu Leu Leu Lys Arg Gly Tyr Leu Thr Ser Ser Ile Ser Ile
166 145             150             155             160
167 Glu Glu Gln Asp Leu Ser Thr Lys Lys Leu Thr Leu Thr Val His Ala
168             165             170             175
169 Gly Lys Val Lys Lys Val Ile Leu Ala Asp Ala Ser Lys Thr Pro Thr
170             180             185             190
171 Tyr Val Lys Ala Ala Ile Pro Leu Lys Phe Asn Gln Ala Phe Arg Leu
172         195             200             205
173 Ser Tyr Leu Glu Gln Gly Leu Asp Asn Leu Lys Arg Ile Asp Pro Thr
174     210             215             220
175 Ala Thr Val Gln Ile Ile Pro Ser Ser Ser Ser Asn Val Ala Asn Asp
176 225             230             235             240
177 Ile Asp Ile Asn Thr Thr Asn Leu Gly Phe Ser Asp Leu Leu Ile Arg
178             245             250             255
179 Met Asp Arg Ser Gln Ser Ala Val Phe Gly Ile Asn Ile Asp Asn Ser
180             260             265             270
181 Leu Ser Lys Asp Tyr Gly Asn Tyr Leu Ile Ser Ala Asn Val Arg Ala
182         275             280             285
183 Asn Asn Leu Met His Leu Asn Asp Glu Trp Asn Leu Ser Ala Asn Tyr
184     290             295             300
185 Pro Leu Ala Arg Leu Ile Asp Ala Ala Gln Asn Asp Leu Gly Val Gln
186 305             310             315             320
187 Val Gly Lys Asp Arg Gln Val Asn Tyr His Ala Ser Leu Thr Ile Pro
188             325             330             335
189 Tyr Gly Leu Tyr Lys Phe Ser Ala Thr His Ser His His Gln Tyr Gln
190             340             345             350
191 Gln Phe Leu Glu Gly Leu His Ala Pro Leu Thr Tyr His Gly Thr Ser
192         355             360             365
193 Lys Thr Ser Ser Ile Gly Leu Ser Arg Leu Leu His Arg Asp Gly Asn
194     370             375             380
195 Gln Lys Thr Glu Gly Tyr Ile Lys Val Asn His Lys Arg Ser Ser Asn
196 385             390             395             400
197 Tyr Ile Asp Asp Val Asn Leu Glu Val Gln Asn Arg Arg Thr Thr Gly
198             405             410             415
199 Tyr Asn Ile Gly Ile Thr His Gln His His Leu His Gln Gly Gly Tyr
200             420             425             430
201 Leu Tyr Ala Asn Leu Asp Tyr Lys Gln Gly Thr Gly Ala Leu Lys Ala
202         435             440             445
203 Lys Pro Ala Pro Glu Glu His Ile Tyr Asp Ala Phe Gly Arg Gln Leu
204     450             455             460
205 Pro Ser Glu Gly Phe Ala Lys Ala Pro Ile Trp Ser Leu Tyr Thr Ser
206 465             470             475             480
207 Phe Gln Lys Pro Phe Val Leu Asn Asn Pro Asn Asp Thr Glu Gln Ala
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208                 485                 490                 495.
209 Gln Asp Lys Ala Thr Ala Asn Lys Pro Ile Tyr Thr Ser Ile Pro Leu
210             500                 505                 510
211 Thr Tyr Thr Ala Arg Leu Gln Ala Gln Tyr Ala Lys Gln Leu Pro Val
212         515                 520                 525
213 Pro Ser Asp Leu Phe Tyr Leu Gly Gly Arg Tyr Ser Ile Lys Gly Ile
214     530                 535                 540
215 Lys Glu Gly Asn Tyr Leu Ser Gly Glu His Gly Phe Ser Leu Ser Gln
216 545                 550                 555                 560
217 Glu Leu Ala Trp Gln Leu Pro Leu Gln Asn Leu Asn Gln His Phe Ser
218             565                 570                 575
219 Thr Asn Ala Asn Ser Ala Gln Leu Tyr Ala Ser Ile Asp Gln Gly Tyr
220             580                 585                 590
221 Ala Tyr Gly Lys Asn Thr Leu Asn Asn Gln Arg His Ile Leu Ala Gly
222         595                 600                 605
223 Ala Val Gly Met Arg Tyr Tyr Phe Gln Gly Ser Gln Asp Pro Arg Ile
224     610                 615                 620
225 Gln Glu Thr Gln Asn Gly Leu Thr His Phe Lys Glu Ser Asn Thr Tyr
226 625                 630                 635                 640
227 Leu Asn Asn Thr Pro Thr Thr Ala His Leu Asp Ile Phe Ile Gly Lys
228             645                 650                 655
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232         675
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235 <211> LENGTH: 1410
236 <212> TYPE: DNA
237 <213> ORGANISM: Moraxella catarrhalis
239 <400> SEQUENCE: 5
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242 catgccttgt atcaagctga tgtcttacaa gcagaatcat tacaaaaatt acactatcct   180
243 aggatatcgc tcaatgcaca cgcctttgta ctgcaacaaa acagcagcat acccttagat   240
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245 gcccccgatg gtctgttgga tgctttgcac aacagcaccc aaaccgccct tgaccgcctg   360
246 cctgaccatc aagatgtcaa gttacgccat gatggcatta ccccaaacat taccgccacg   420
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248 cagcgtggta aatttggatt acaagaacgc atctctttgg caaaacttaa tttgattcgc   540
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250 gccatgcagt acatgtagta atgcttat aaattagaac agcaaggttt tatcagtcgt   660
251 ggacagcgta tgcaatttga agtggcacgc aatcaggtac aaagactgta tcaaagcacc   720
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253 gaaccgctaa gcacaccgct gtttatcaac acccagcatc gccccaattg gcaagcatta   840
254 ctcaaagact cccaaaatac accattaaat caaaagctaa aaaccgacat tttgcttgcc   900
255 gatgaaaata tcgccctaag acaatccacc aaaaaaccaa aaattgccgc tgtggctcgt   960
256 tataccttag atgataagcc tgattggttt gcaggtgtgg cggtttctta caacctattc  1020
257 ttgggcattg accgtgataa gcagattggg gcagcacacc tacaaaaaca agcagcccaa  1080
258 ttgggtcatg aacaagtcaa tgaacacatc acaaccacca tgcacaccgc ttatggcgag  1140
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VERIFICATION SUMMARY
PATENT APPLICATION: US/10/088,046

DATE: 04/04/2002
TIME: 15:38:36

Input Set : **A:\seqlist.txt**
Output Set: **N:\CRF3\04042002\J088046.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date